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GenCore version 5.1.3
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OM protein - nucleic search, using frame_plus_p2n model

Run on: November 9, 2002, 04:42:12 ; Search time 69 seconds
(without alignments)
844.472 Million cell updates/sec

Title: US-09-895-298A-83
Perfect score: 1002
Sequence: 1 MMNFQPSKAMRASQMTFF.....HDSLDIRSRVQEGNPRA 190

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 441362 segs, 15338381 residues
Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+L2n.model -DEV=xlp
-O=/cgn2.1/USPTO_SPOOL/US09895298/runat_06112002_160416_2357/app_query.fasta_1.327
-DB=Issued_Patents_NA -QEMT=fastap -SUFFIX=trn1 -MINMATCH=0.1 -LOOPCL=0
-DOEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blomsum62 -TRANS=human40.cdi
-LIST=45 -DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptio -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09895298 -EGCN_1.1_31.etrnat_06112002_160416_2357 -NCPU=6 -ICPU=3
-NO_XLPRX -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV.TIMEOUT=120
-WARN.TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

- 1: Issued_Patents_NA.*
- 2: /cgn2.6/ptodata/1/ina/5A.COMB.seq.*
- 3: /cgn2.6/ptodata/1/ina/5B.COMB.seq.*
- 4: /cgn2.6/ptodata/1/ina/6A.COMB.seq.*
- 5: /cgn2.6/ptodata/1/ina/6B.COMB.seq.*
- 6: /cgn2.6/ptodata/1/ina/PCRTUS.COMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	88	8.8	4403765	4 US-09-103-840A-2	Sequence 2, Appli
2	88	8.8	4411529	4 US-09-103-840A-1	Sequence 1, Appli
3	86	8.6	1581	2 US-08-843-998-1	Sequence 1, Appli
4	86	8.6	1581	3 US-09-206-537-1	Sequence 1, Appli
5	86	8.6	1581	4 US-09-430-854-1	Sequence 1, Appli
6	85	8.5	1168	4 US-08-858-207A-182	Sequence 182, App
7	82.5	8.2	40000	4 US-09-780-049-18	Sequence 18, Appli
8	80	8.0	2555	2 US-08-693-457-3	Sequence 3, Appli
9	80	8.0	2555	4 US-09-265-731-3	Sequence 3, Appli
10	79.5	7.9	450	4 US-09-235-451-11	Sequence 11, Appli
11	79	7.9	1491	4 US-09-134-001C-164	Sequence 164, App
12	78.5	7.8	1812	4 US-09-008-097-3	Sequence 3, Appli

13	78.5	7.8	3549	4 US-09-008-097-5	Sequence 5, Appli
14	78	7.8	2243	1 US-07-995-657-1	Sequence 1, Appli
15	78	7.8	2243	1 US-08-474-587-1	Sequence 1, Appli
16	78	7.8	10254	4 US-08-961-527-29	Sequence 29, Appli
17	77.5	7.7	4255	5 PCT-US96-02331-14	Sequence 14, Appli
18	77.5	7.7	4835	1 PCT-US96-02331-9	Sequence 9, Appli
19	77.5	7.7	4835	5 PCT-US96-02331-9	Sequence 39, Appli
20	77.5	7.7	7186	4 US-08-961-527-39	Sequence 9, Appli
21	77.5	7.7	8543	3 US-08-496-944-1	Sequence 1, Appli
22	76.5	7.6	2713	4 US-08-285-439-1	Sequence 1, Appli
23	76	7.6	4942	1 US-09-474-076-1	Sequence 1, Appli
24	75.5	7.5	939	4 US-09-302-769-35	Sequence 35, Appli
25	75.5	7.5	848	4 US-09-134-001C-621	Sequence 621, App
26	75	7.5	1401	4 US-09-134-001C-183	Sequence 183, App
27	75	7.5	2352	2 US-08-889-909A-21	Sequence 21, Appli
28	75	7.5	2352	4 US-09-156-163A-21	Sequence 21, Appli
29	75	7.5	2602	4 US-08-838-151A-17	Sequence 17, Appli
30	75	7.5	4881	4 US-08-961-527-125	Sequence 125, App
31	75	7.5	16442	3 US-08-781-891-208	Sequence 208, App
32	74.5	7.4	893	1 US-08-276-452A-66	Sequence 66, Appli
33	74.5	7.4	893	2 US-08-798-744-66	Sequence 66, Appli
34	74	7.4	1209	4 US-08-791-115B-24	Sequence 24, Appli
35	74	7.4	1962	4 US-08-791-115B-3	Sequence 3, Appli
36	74	7.4	3224	4 US-08-965-729A-2	Sequence 2, Appli
37	73.5	7.3	1101	4 US-09-134-001C-2665	Sequence 2665, Ap
38	73.5	7.3	1239	4 US-09-134-001C-1112	Sequence 1112, Ap
39	73.5	7.3	2225	4 US-09-276-531-109	Sequence 109, App
40	73	7.3	1491	1 US-08-137-614A-3	Sequence 3, Appli
41	73	7.3	1491	2 US-08-768-301-1	Sequence 1, Appli
42	73	7.3	3518	4 US-09-412-210-2	Sequence 2, Appli
43	72.5	7.2	2079	2 US-08-990-114-2	Sequence 2, Appli
44	72.5	7.2	2079	4 US-09-241-333-2	Sequence 2, Appli
45	72.5	7.2	3357	3 US-08-726-214-7	Sequence 7, Appli

ALIGNMENTS

US-09-103-840A-2
RESULT 1
Sequence 2, Application US/09103840A
Patent No. 6294328
GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
TITLE OF INVENTION: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 4403765
TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
FEATURE:
OTHER INFORMATION: CDC 1551
OTHER INFORMATION: "a" bases at various positions throughout the sequence
US-09-103-840A-2
Alignment Scores:
Pred. No.: 3.64e+04
Score: 88.00
Percent Similarity: 47.62%
Best Local Similarity: 30.95%
Query Match: 8.788
DB: 4
US-09-895-298A-83 (1-190) x US-09-103-840A-2 (1-4403765)
Length: 4403765
Matches: 26
Conservative: 14
Mismatch: 32
Indels: 12
Gaps: 4

Oy 6 ProPseRlysAlaTrpAry-----AlaserInmetThrphePheleu 23
 |||||
 Db 207713 CCGCGGGCAGCCGCTGGCGGTGTATGCGCTGTCTGCTGGATTGACCATTCTCTT 207772
 Oy 24 -----LeuphePheproSerPheThrgIvalLeuCystrIleuAlaIle 38
 |||||
 Db 207773 CTGGCGGTAAACCGGTGTGTGTCTGTCCGACGATGACCGGATGGAGTCTTGGCCGCGCTCTT 207833
 Oy 39 ThrIeTrpArgLeu-----LysProSerAlaspGyGlyProPheArgIleuPro 56
 |||||
 Db 207833 ACCGGCATCCGGGTGTGTGCGCGTGACGCGCTCCGCCATCGGTCCGTGGCG----- 207883
 Oy 57 LeupheIleIleSerIleTySerTrpIleAspThrIleuSerThrArgProGlyTyTrpLeu 76
 |||||
 Db 207884 TTGGGTGTCCGGGATTTGGCCACACTGTGGTGACACCCCTCTGGCTGTGGGTGGCTG 207943
 Oy 77 TrpValValTrp 80
 |||||
 Db 207944 TGGCGCGTGTGG 207955

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RESULT 2
US-09-103-840A-1
: Sequence 1, Application US/09103840A
: Patent No. 6294328
: GENERAL INFORMATION:
: APPLICANT: FLEISCHMAN, Robert D.
: APPLICANT: WHITE, Owen R.
: APPLICANT: FRASER, Claire M.
: APPLICANT: VENTER, John C.
: TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
: TITLE OF INVENTION: TUBERCULOSIS
: FILE REFERENCE: 24366-20007.00
: CURRENT APPLICATION NUMBER: US/09/103,840A
: CURRENT FILING DATE: 1998-06-24
: NUMBER OF SEQ ID NOS: 2
: SOFTWARE: Patentln Ver. 2.1
: SEQ ID NO 1
: LENGTH: 4411529
: TYPE: DNA
: ORGANISM: Mycobacterium tuberculosis
: OTHER INFORMATION: H37Rv
US-09-103-840A-1

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[illegible]

US-09-895-298A-83 (1-190) x US-09-103-840A-1 (1-4411529)

Oy	6	ProPserSerlyAlaIleTrrArg-----AlasergImeMethrPhrheHeilePhelen	23
Db	207603	CCCCGGGACAGCGCGATGGCGGGGTATTACCGETCTGCTCTGCATTTAGACAACTTCCTTT	207662
Oy	24	-----LeuphePherProSerPhetrhGlyValIleucYstrIleualaIle	38
Db	207663	CTGGCCGTTAACCGGATGTGTTTGCCGAGACTTCCGAGATTGAGNTTGTGGCCGCTCCTT	207722
Oy	39	ThrIleTrrArgLyu-----LysProserAlaAspCyGlyProheaArgGlyLeupro	56
Db	207723	ACCGGCAATCCGGGATGGTTCGGCGGTACAGCGCTCCGCATGTGGTCCTGGGGGG-----	207773
Oy	57	LeupheHeileHsserIleTyfiserTrpIleaAsprhIleuerThnarApGrOglyTyrlau	76
Db	207774	TTCGCTGCCCGGGAATTTCGCGACAATTGTGGACACCCTCTCGCTGTTTTGNGGATGGCTG-207833	207833
Oy	77	TrpValValTrr	80
Db	207834	TGGCCGCTGTGG	207845

```

1      RESULT 3
2      US-08-845-998-1/c
3      Sequence 1 Application US/08845998
4      Patent No. 5878892
5      GENERAL INFORMATION:
6      APPLICANT: Van Baren, Nicolas
7      APPLICANT: Coulie, Pierre G.
8      APPLICANT: De Smet, Charles
9      APPLICANT: Lucas, Sophie
10     APPLICANT: Boon, Thierry
11     TITLE OF INVENTION: LEUKEMIA ASSOCIATED GENES
12     NUMBER OF SEQUENCES: 16
13     CORRESPONDENCE ADDRESS:
14     ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
15     STREET: 600 Atlantic Avenue
16     CITY: Boston
17     STATE: MA
18     COUNTRY: US
19     ZIP: 02210
20     COMPUTER READABLE FORM:
21     MEDIUM TYPE: Floppy disk
22     COMPUTER: IBM PC compatible
23     OPERATING SYSTEM: PC-DOS/MS-DOS
24     SOFTWARE: Patent In Release #1.0, Version #1.25
25     CURRENT APPLICATION DATA:
26     APPLICATION NUMBER: US/08/845,998
27     FILING DATE:
28     CLASSIFICATION: 435
29     ATTORNEY/AGENT INFORMATION:
30     NAME: Van Amsterdam, John R.
31     REGISTRATION NUMBER: 40,212
32     REFERENCE/DOCKET NUMBER: L0461/7008
33     TELECOMMUNICATION INFORMATION:
34     TELEPHONE: (617)720-3500
35     TELEFAX: (617)720-2441
36     INFORMATION FOR SEQ ID NO: 1:
37     SEQUENCE CHARACTERISTICS:
38     LENGTH: 1581 base pairs
39     TYPE: nucleic acid
40     STRANDEDNESS: double
41     TOPOLOGY: linear
42     MOLECULE TYPE: cDNA
43     HYPOTHETICAL: NO
44     ANTI-SENSE: NO
45     FEATURE:
46     NAME/KEY: CDS
47     LOCATION: 106..831
48     US-08-845-998-1

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Alignment Scores:	
Pred. No.:	0.299
Score:	86.00
Percent Similarity:	39.928
Best Local Similarity:	22.658
Query Match:	6.588
DBs:	2

US-09-895-2984-83 (1-190) x US-08-845-998-1 (1-1581)

[illegible]

Sequence 1, Application US/09430854
Patent No. 6271019
GENERAL INFORMATION:
APPLICANT: Van Baren, Nicolas
APPLICANT: Coulie, Pierre G.
APPLICANT: De Smet, Charles
APPLICANT: Lucas, Sophie
TITLE OF INVENTION: LEUKEMIA ASSOCIATED GENES
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
STREET: 600 Atlantic Avenue
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/430,854
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/845,998
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Van Amsterdam, John R.
REGISTRATION NUMBER: 40,212
REFERENCE/DOCKET NUMBER: L0461/7008
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)720-3500
TELEFAX: (617)720-2441
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1581 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 106..831
US-09-430-854-1

Alignment Scores:
Pred. No.: 0.299 Length: 1581
Score: 86.00 Matches: 54
Percent Similarity: 39.928 Conservative: 41
Best Local Similarity: 22.698 Mismatches: 65
Query Match: 8.58% Indels: 78
Gaps: 16

US-09-895-298A-83 (1-190) x US-09-430-854-1 (1-1581)

QY 11 TTPARGALASerGlnMetMetThrPhePheIlePheLeuLeuPhePheProSerPheThr 30
Db 654 TTGAGCATCAGGTCCT 595
QY 31 GtYVal---LeucYsthrIleuAlaIleThrIleThrArgLeuYsProSerAlaAspCys 49
Db 594 AGCCTTGAGTCCTGACGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 538
QY 50 -----GlyProPheArgGlyLeuProLeuPheIleHisSerIleYrSerTrp 65
Db 537 AACCCAGGGGAGCCGCCGCCAGAGATGCTCCGCTT-----GTCGCGGCTTAC 490
QY 66 IleAsp-----ThrLeuSerThrArgProGlyTyrLeuTrp 77

Db 489 ATCAGTCAGACCATGAAAGCCTCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 442
QY 78 ValValTrpIleYrArgAsnLeuIleGlySerValHis-----Phe 91
Db 441 -----TTTGTGGGTTC---CACAGCCCCCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 406
QY 92 PhePheIleLeuThrIleuAlaIleThrIleThrArgLeuYsProSerAlaAspCys 111
Db 405 CTCTCTCTCAAGCCCT 349
QY 112 GtYArgIleMetIleArgLeuLeuHisGlnIleIleAsn-----126
Db 348 GGAAGCCAGCTCAGATTGAAGAATCTGGGACGGGAGCTCTCACCCCTGCTCCCTTGCAG 289
QY 127 -----GtYArgIleMetIleArgLeuLeuHisGlnIleIleAsn-----126
Db 288 CCGCTGATGTTTTCCTGAGGAG 229
QY 141 LeuGlnAspMetGluYsLys-----147
Db 228 GCCCGATGCTCCGCGGCGCTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 169
QY 148 AlaAsnProSerSerLeuValLeuGluArgGluValGlnGln-----Gly 164
Db 168 GCCGGGAGACCGGTGAGGTTCAGGTCAGAACGACGACGACGACGACGACGACGACGACGACG 109
QY 165 PheLeuHisLeuGly-----GluHisAspGlySer-----174
Db 108 -----CATCGCGCGCTCTCCAGAGTGGGCTCCACAGAGATGGTCCGGAGATCCGGGGA 55
QY 175 LeuAspLeuArgSerArg-----ArgSerValGlnGlnGlnGlnProArgAla 190
Db 54 CTGGGATCCGAGTCGCGAGTCAGAGATCTGACAGCGCTGACAGCGCTGACAGCGCGGGG 1

RESULT 6
US-08-858-207A-182/c
Sequence 182, Application US/08858207A
Patent No. 6348328
GENERAL INFORMATION:
APPLICANT: Black, Michael
APPLICANT: Hodgson, John
APPLICANT: Knowles, David
APPLICANT: Nicholas, Richard
APPLICANT: Stodola, Robert
TITLE OF INVENTION: No. 6348328el Compounds
NUMBER OF SEQUENCES: 552
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/858,207A
FILING DATE: 09-MAY-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/017670
FILING DATE: 14-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Glimm, Edward R.
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P50475
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090


```

Db 345 GGTGGGGTTCACGGCCGGAAGCAAGATGACTCCGGGTGGTTCAGAGGTGATGAGT 404
QY 186 yasn 187
   |||
Db 405 GAAC 408

RESULT 11
US-09-134-001C-164
; Sequence 164, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC
; FILE REFERENCE: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; CURRENT APPLICATION NUMBER: US/09/134,001C
; PRIOR FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 164
; LENGTH: 1491
; TYPE: DNA
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-164

Alignment Scores:
Pred. No.: 2.19 Length: 1491
Score: 79.00 Matches: 37
Percent Similarity: 39.63% Conservative: 28
Best Local Similarity: 22.56% Mismatches: 45
Query Match: 7.88% Indels: 54
                Gaps: 8

US-09-895-298A-83 (1-190) x US-09-134-001C-164 (1-1491)
QY 27 ProserPheThnGlyValLeuCystrHeuAlaIleThrIleTyrPargLeuLysProser 46
   ||| ||| :||| :||| :||| :||| :|||
Db 553 CCTATATTTCAGTATTATATGATCATGATGATGATTCATTCACCTCAGACTTAAATCC 612
QY 47 AlaaspCysGlyProPheArgGlyLeuProLeuPheIleHisSerIleTyrSerTrpIle 66
   ||| ||| :||| :||| :||| :||| :|||
Db 613 GGT-----TTTATGATGATGACAGTGAAGTGTGGCGTTTAACTTGAAGTGGGA 660
QY 67 AsphTrleUser-----ThrArgProGlyTyrIleuTrpValValITrPileTyrArgAsnLeu 85
   ||| ||| :||| :||| :||| :||| :|||
Db 661 GATCAAAAGGGCAAGCAATAAAGTACTATGTGTAGTAACTGATGGTATTCACAGGGGATT 720
QY 86 IleGlySerValHisPhe-----PhePhe 93
   ||| :||| |||
Db 721 GAAGGAGCGCGTTGCTTTTCGACGTGCAAAAGTCAAAAGAGTGAAGACTGCTAC 780
QY 94 IleleuTrleuIle---ValleuIleIleThrTyrIleuTyrTrpGlnIleThrGluGly 112
   :||| :||| :||| :||| :||| :||| :|||
Db 781 GTTATTGGTTGATTCTGTGCTAGTCATTTATTCTTAATGACAGCTAGTACCCAAAGT 840
QY 113 ArgGlyIleMetIleArgLeuLeuHisGluGlnIleIleAsnGluGlyLysAspLysMet 132
   :||| :||| :||| :||| :||| :||| :|||
Db 841 -----GTCATTCACCAAGCAAAATTTCA----- 864
QY 133 PheIleuIleGluLysLeuIleLysLeuGlnAspMetGluLysAlaAsnProser--- 151
   ||| ||| ||| ||| ||| ||| |||
Db 865 -----AAACTTTCCTAAATCCATCAATG 885
QY 152 SerLeuValLeuGluArgArgGluValGluGlnGlnGlyPheLeuHisLysGlyGluHis 171
   :||| :||| :||| :||| :||| :||| :|||
Db 886 GCACAAAGATTAAGAA-----CATATTGTAGTGCAT 915
QY 172 AspGlySerLeu 175
   ||| ||| :||| :||| :||| :|||
Db 916 TGGGGTTCAGTG 927

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RESULT 12
US-09-008-097-3
Sequence 3, Application US/09008097
Patent No. 6306830
GENERAL INFORMATION:
APPLICANT: Hammond, H. Kirk
APPLICANT: Insel, Paul A.
APPLICANT: Ping, Peipei
APPLICANT: Post, Steven R.
APPLICANT: Gao, Melina
TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE
HEART FAILURE
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CITY: PALO ALTO
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/008,097
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Dylan, Tyler M
REGISTRATION NUMBER: 37,612
REFERENCE/DOCKET NUMBER: 22000-20567.21
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-813-5600
TELEFAX: 650-494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1812 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 1...1812
OTHER INFORMATION:
US-09-008-097-3
Alignment Scores:
Pred. No.:          3.45      Length:      1812
Score:              78.50     Matches:    42
Percent Similarity: 40.33%   Conservative: 31
Best Local Similarity: 23.20% Mismatches: 63
Query Match:        7.83%    Indels:     45
DB:                  4       Gaps:       8
US-09-0895-298A-83 (1-190) x US-09-008-097-3 (1-1812)
QY      30  ThisGValleuuhsrileuhalalierhrllertpargleuluysproser-----Alaas 48
Db      83  TCtGGgGCCCTGTgtTCttTGrATACatCGCATACAGCCCTCCCAATCGCATGCGGG 143
QY      48  pCYsglyProPhearGlyLeuProLeuPhe-IleHisserIletysetrrlilaspr 68
Db      143  ctGCcGcttCCACAGGCGCGGGGcTtCCACCtTGcATTtATCTtgGcCTGG-----C 196
QY      68  hrLseetThrarPrroglYtyrLeutrrPvalvairPlietyrarGaInleuegllys 88

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Db 197 AACCTTAACCGTGGGATGAGCCCTTCTCTGG-----AACGAGCTGGTG 238
Qy 88 erValHisPhePhePheIleuThrIleuIleValIleuIleIleThrTyrIleuTyrTrpG 108
Db 239 CCAATGTGCTCTGTCTCTCTCGACCAACGTCATTAACATCTGACACACATATCCAGC 298
Qy 108 IuIleThr-----GluGlyArgGlySIleMetIleArgIleuIleHisG 122
Db 299 AGGTGTCTCAGCCGACGCCCTTTCAGAGACCGCAGTTCATATCCAGCCCGGCTCCACC 358
Qy 122 IuGluIleIleAsnGluGlyLysAspLysMetPheIleuIleGluLysIleuIleLysLeuG 142
Db 359 TGCACGATGAAATATCGGCAGAGAGAGCGGCTGCGTGTG----- 366
Qy 142 IAspMetGluLysLysAlaAsnProSerSerIleuValIleuGluArgGlu----- 159
Db 397 -----TCGGTATTGCCCCAGCACGTTGCCATGGAGATGAAGAAGACATCA 442
Qy 160 --ValGluGlnGlnGlyPheIleuHis-----LeuGlyGluHisAsp----- 172
Db 443 ACACAAAAAAGAGACATGTTCCACAAATCTATACATGACAGAAAGCAACAATGTCCAGCA 502
Qy 173 -----GlySerLeuAspIleuArgSerArgSerValGlnGlu 185
Db 503 TCTCTGTTTGCAGACATGAGGGCTTCCACACGCTGGCATGCCATGCCATGCCAGTCCG 561

RESULT 13
US-09-008-097-5
: Sequence 5, Application US/09008097
: Patent No. 6306830
: GENERAL INFORMATION:
: APPLICANT: Hammond, H. Kirk
: APPLICANT: Insel, Paul A.
: APPLICANT: Pingel, Peidel
: APPLICANT: Post, Steven R.
: APPLICANT: Gao, Meihua
: TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE
: TITLE OF INVENTION: HEART FAILURE
: NUMBER OF SEQUENCES: 9
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: MORRISON & FOERSTER
: STREET: 755 PAGE MILL ROAD
: CITY: PALO ALTO
: STATE: CA
: COUNTRY: USA
: ZIP: 94304-1018
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette
: COMPUTER: IBM Compatible
: OPERATING SYSTEM: DOS
: SOFTWARE: FastSeq for Windows Version 2.0
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/008,097
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER:
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Dylan, Tyler M
: REGISTRATION NUMBER: 37,612
: REFERENCE/DOCKET NUMBER: 22000-20567.21
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 650-813-5600
: TELEFAX: 650-494-0792
: TELEX: 706141
: INFORMATION FOR SEQ ID NO: 5:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 3549 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: FEATURE:

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NAME/KEY: Coding Sequence
 LOCATION: 1...3501
 OTHER INFORMATION:
 US-09-008-097-5

Alignment Scores:
 Pred. No.: 9.8 Length: 3549
 Score: 78.50 Matches: 42
 Percent Similarity: 40.33% Conservative: 31
 Best Local Similarity: 23.20% Mismatches: 63
 Query Match: 7.83% Indels: 45
 DB: 4 Gaps: 8

US-09-895-298a-83 (1-190) x US-09-008-097-5 (1-3549)

QY 30 ThrGlyValLeuCyStHleuAlaIleThrIleTrpAlaGlyuProSer-----AlaAs 48
 Db 716 TCTGTGCGCTGCTGCTTCTTGTATACATCGATACACGCTCTCCATCCGATCGCGG 775
 QY 48 PCysGlyProPheArgGlyLeuProLeuPhe-IleHisSerIleTyrSerTrpIleAsp 68
 Db 776 CTGCGCTCTCAGCGGCTGGGCTCTCCACCTTGCACTTGAATCTGGCTGG-----C 829
 QY 68 hrlSerThrArgProGlyTyrLeuTrpValIleTrpIleTyrArgAsnLeuIleGlyS 88
 Db 830 AACTTAACCGTGGTGCATGCTCTGCTG-----AAGCAGCTCGGTG 871
 QY 88 erValHisPhePheIleLeuThrIleValLeuIleIleThrTyrLeuTyrTrpG 108
 Db 872 CCAATGTGCTGCTGCTCTGCAACCAAGTCATTCATTCGACATATCCAGCAG 931
 QY 108 InIleThr-----GluGlyArgGlyIleMetIleArgLeuLeuHisG 122
 Db 932 AGGTGCTCAGCCCGGCTTTCAGAGACCGGATGATACATCAGGCCGCGCTCCACC 991
 QY 122 IuGlnIleIleAsnGluGlyAspIleMetPheLeuIleGluGlyLeuIleGlyLeuG 142
 Db 992 TGCAAGCATGAAATCGGACGAGAGCGGCTGCTG-----1029
 QY 142 InAspMetGluGlyLysAlaAsnProSerSerLeuValLeuGluArgArgGlu----- 159
 Db 1030 -----TCGGTATTGCCCGCCAGCAGCTGCGCATGGAAGAAAGACATCA 1075
 QY 160 --ValGluGlnGlnGlyPheLeuHis-----LeuGlyGluHisAsp----- 172
 Db 1076 ACACAAAAGAGAGATGTTCCACAAGATCTACATACAGAGCATGACATATGTCACGA 1135
 QY 173 -----GlySerLeuAspLeuArgSerArgArgSerValGlnGlu 185
 Db 1136 TCCTGTTTCAGACATTCAGAGGCTTCACACGCTGCGCATCCAGTGCACCTGCGCAGAG 1194

RESULT 14
 US-07-995-657-1
 Sequence 1, Application US/07995657
 Patent NO. 5443974

GENERAL INFORMATION:
 APPLICANT: Hitz, William D.
 APPLICANT: Yadev, Narendra S.
 APPLICANT: Perez-Grau, Luis
 TITLE OF INVENTION: Nucleotide Sequence of
 TITLE OF INVENTION: Soybean Stearoyl-ACP
 TITLE OF INVENTION: Desaturase cDNA
 NUMBER OF SEQUENCES: 7
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: E. I. du Pont de Nemours
 ADDRESSEE: and Company
 STREET: 1007 Market Street
 CITY: Wilmington
 STATE: Delaware
 COUNTRY: U.S.A.
 ZIP: 19898
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.50 inch, 1.0 MB

COMPUTER: Macintosh
 OPERATING SYSTEM: Macintosh System, 6.0
 SOFTWARE: Microsoft Word, 4.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/995,657
 FILING DATE: 19921211
 FILING DATE: C) CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: GEIGER, KATHLEEN W.
 REGISTRATION NUMBER: 35,880
 REFERENCE/DOCKET NUMBER: BB_1022-B
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 302-892-8112
 TELEFAX: 302-892-7949
 TELETYPE: 835420
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2243 base pairs
 TYPE: NUCLEIC ACID
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA to mRNA
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 ORGANISM: Glycine max
 STRAIN: Cultivar Wye
 DEVELOPMENTAL STAGE: Developing seeds
 IMMEDIATE SOURCE:
 LIBRARY: cDNA to mRNA
 CLONE: pDS1
 FEATURE:
 NAME/KEY: 5' non-coding sequence
 LOCATION: 1..69
 OTHER INFORMATION: /note="IDENTIFICATION
 OTHER INFORMATION: METHOD-Deduced by proximity to location 70-72"
 FEATURE:
 NAME/KEY: Putative translation initiation codon
 LOCATION: 70..72
 OTHER INFORMATION: /note="IDENTIFICATION
 OTHER INFORMATION: METHOD-Similarity of the context of the
 OTHER INFORMATION: methionine codon in the open reading frame to
 OTHER INFORMATION: translation
 FEATURE:
 NAME/KEY: Putative transit peptide coding sequence
 LOCATION: 70..165
 OTHER INFORMATION: /note="IDENTIFICATION
 OTHER INFORMATION: METHOD-Deduced by proximity to location 70-72
 OTHER INFORMATION: and location 166-1242"
 FEATURE:
 NAME/KEY: Mature protein coding sequence
 LOCATION: 166..1242
 OTHER INFORMATION: /note="IDENTIFICATION
 OTHER INFORMATION: METHOD-Experimental determination of N-terminal
 OTHER INFORMATION: amino acid sequence and subunit size of
 OTHER INFORMATION: purified soybean
 FEATURE:
 NAME/KEY: Translation termination codon
 LOCATION: 1243..1245
 OTHER INFORMATION: /note="IDENTIFICATION
 OTHER INFORMATION: METHOD-The translation codon ends the open
 OTHER INFORMATION: reading frame for a protein of the expected
 OTHER INFORMATION: size"
 FEATURE:
 NAME/KEY: 3' non-coding sequence
 LOCATION: 1246..2243
 OTHER INFORMATION: /note="IDENTIFICATION
 OTHER INFORMATION: METHOD-Established by proximity to location
 OTHER INFORMATION: 1243-1245"
 US-07-995-657-1

Alignment Scores:

Pred. No.:	5.57	Length:	2243
Score:	78.00	Matches:	43
Percent Similarity:	34.63%	Conservative:	28
Best Local Similarity:	20.98%	Mismatches:	56
Query Match:	7.78%	Indels:	78
DB:	1	Gaps:	9

US-09-895-298a-83 (1-190) x US-07-995-657-1 (1-2243)

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QY 19 PhePheIlePheLeuLeuPhePheProSerPheThrGlyValLeuGlyThrLeu----- 36
    ||| |||||::: ||||| ||| |||||:::
Db 1324 TTGTGATTTTATCTTTTCTTCTCTGTTTGTG---GTCTATGTTATATCCACTG 1380
QY 37 -----AlaIleThrIleTrp-----Arg 42
    ::| |||
Db 1381 TAAGTGAACAGCTGTTCTTGCATGTTGCAAGTTAAGCACTTAAGGGCAGCTGAGT 1440
QY 43 LeuLysProSerAlaAspGlyProPheArgGlyLeuProLeuPheIleHisSerIle 62
    ::|::: ||| |||||
Db 1441 ATTGAAGATGCTATTTTGTGTTCCCTTTT----- 1470
QY 63 TyrSerTrpIleAspThrLeuSerThrArgProGlyTyrLeuTrp-----ValValTrp 80
    ||||| |||||
Db 1471 -----CTGTGTAGTATGATCTGTGTG 1491
QY 81 IleTyrArgAsnLeuIleGlySerValHisPhePheIleLeuThrLeuIleValLeu 100
    |||||::: ||| ::|:::
Db 1492 AAGTATTAAGTAACG-----TTTTTTTCTCTGCAATTTTGAATGATGA 1536
QY 101 IleIleThrTyrLeuYrTrpGlnIleThrGlnGlyArgLysIle----- 115
    ::|::|::|
Db 1537 -----AAGAAATTTAGTTCTTAACACG 1560
QY 116 -----MetIleArgLeuLeuHisGlnIle 124
    ::|:::
Db 1561 TCGCACCTTCCCTGAGGCTTCTGTCTGTCCGAGTACCATGCTGAGGTTAGTGTG 1620
QY 125 IleAsnGlnGlyLysAspLysMetPheLeuIleGlnLysLeuIleLysLeuGlnAspMet 144
    ::|::|::: ||||| ||| |||
Db 1621 CTGAACGATGCTCTGAAGACATGCTCAATGCTGAGAAAGGCAAGCCCAAGTCATG 1680
QY 145 GlnLysLysAlaAsnProSerSerLeuValLeuGlnArgGlnValGlnGlnGlnGly 164
    |||||::: |||:::
Db 1681 -----ATTGCGCATCTCTCAAGTCATTCAAATTCCTTTGTGATGCAGAG 1731
QY 165 PheLeuHisLeuGlyLysHisAspGlySerLeuAspLeuArgSerArgSerValGln 184
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QY 185 GlnGlyAsnProArg 189
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Db 1792 GAATTGAACGGTAGA 1806

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RESULT 15

US-08-474-587-1

Sequence 1, Application US/08474587

Patent No. 5760206

GENERAL INFORMATION:

APPLICANT: Hiltz, William D.

APPLICANT: Perez, Luis

TITLE OF INVENTION: Nucleotide Sequence of

Patent No. 5760206

TITLE OF INVENTION: Soybean Stearoyl-ACP

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSEE: E. I. du Pont de Nemours

STREET: 1007 Market Street

CITY: Wilmington

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STATE: Delaware
COUNTRY: U.S.A.
ZIP: 19898
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.0 MB
COMPUTER: Macintosh
OPERATING SYSTEM: Macintosh System, 6.0
SOFTWARE: Microsoft Word, 4.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,587
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: SIEGELL, BARBARA C.
REGISTRATION NUMBER: 30,684
REFERENCE/DOCKET NUMBER: BB_1022-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-992-4931
TELEFAX: 302-773-0164
TELEX: 835420
INFORMATION FOR SEQ. ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2243 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: glycine max
STRAIN: Cultivar Wye
DEVELOPMENTAL STAGE: Developing seeds
IMMEDIATE SOURCE:
LIBRARY: cDNA to mRNA
CLONE: pDS1
FEATURE:
NAME/KEY: 5' non-coding sequence
LOCATION: 1..69
OTHER INFORMATION: /note="IDENTIFICATION"
OTHER INFORMATION: METHOD-Deduced by proximity
OTHER INFORMATION: to location 70-72"
FEATURE:
NAME/KEY: Putative translation initiation codon
LOCATION: 70..72
OTHER INFORMATION: /note="IDENTIFICATION"
OTHER INFORMATION: METHOD-Similarity of the
OTHER INFORMATION: context of the methionine
OTHER INFORMATION: codon in the open reading frame to translation
FEATURE:
NAME/KEY: Putative transit peptide coding sequence
LOCATION: 70..165
OTHER INFORMATION: /note="IDENTIFICATION"
OTHER INFORMATION: METHOD-Deduced by proximity
OTHER INFORMATION: to location 70-72 and
OTHER INFORMATION: location 166-1242"
FEATURE:
NAME/KEY: Mature protein coding sequence
LOCATION: 166..1242
OTHER INFORMATION: /note="IDENTIFICATION"
OTHER INFORMATION: METHOD-Experimental
OTHER INFORMATION: determination of N-terminal
OTHER INFORMATION: amino acid sequence and subunit size of purified soybean
FEATURE:
NAME/KEY: Translation termination codon
LOCATION: 1243..1245
OTHER INFORMATION: /note="IDENTIFICATION"
OTHER INFORMATION: METHOD-the translation
OTHER INFORMATION: codon ends the open reading
OTHER INFORMATION: frame for a protein of the expected size"

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FEATURE:
; NAME/KEY: 3' non-coding sequence
; LOCATION: 1246..2243
; OTHER INFORMATION: /note= "IDENTIFICATION
; OTHER INFORMATION: METHOD=Established by
; OTHER INFORMATION: proximity to location
; OTHER INFORMATION: 1243-1245"
US-08-474-587-1
```

Alignment Scores:

Pred. No.:	5.57	Length:	2243
Score:	78.00	Matches:	43
Percent Similarity:	34.63%	Conservative:	28
Best Local Similarity:	20.98%	Mismatches:	56
Query Match:	7.78%	Indels:	78
DB:	1	Gaps:	9

US-09-895-298a-83 (1-190) x US-08-474-587-1 (1-2243)

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QY 19 PhePheIlePheLeuPhePheProSerPheThrGlyValLeuCysThrLeu----- 36
    ||| |||||::: ||||| ||| |||||:::
Db 1324 TTGTCATTTTATCTTTTTCCTGCTTTTG---GTCCTATGTTATATGCCACTG 1380

QY 37 -----AlaIleThrIleTrp-----Arg 42
    ::| |||
Db 1381 TAAGGTGAACAGTGTCTTCGCAATGTAAGCAGTTAGGGCAGCTGTAGT 1440

QY 43 LeuLysProSerAlaAspCysGlyProPheArgGlyLeuProLeuPheIleHisSerIle 62
    ::::: ::| ||| |||||
Db 1441 ATTGAAATGCTATTTTGTTCCTCTTT----- 1470

QY 63 TyrSerTrpIleAspThrLeuSerThrArgProGlyTyrLeuTrp-----ValValTrp 80
    |||||
Db 1471 -----CTGTGTAGTATGCTGTGG 1491

QY 81 IleTyrArgAsnLeuIleGlySerValHisPhePheIleLeuThrLeuIleValLeu 100
    ::::: ||||| ||| :::::
Db 1492 AAGTATAGTAAACG-----TTTTCCTGCGCAATTTGATGATA 1536

QY 101 IleIleThrTyrLeuTyrTrpGlnIleThrGlnGlyArgGlySile----- 115
    ::|||
Db 1537 -----AAGAAATTTAGTTCTTAAACCG 1560

QY 116 -----MetIleArgLeuLeuHisGlnIle 124
    :::::
Db 1561 TCGCACCTCCCTGAGGCTTCTTGTCTGTCGCGAGTGACCATGTTGAGGTTAGTGTG 1620

QY 125 IleAsnGlnGlyLysAspLysMetPheLeuIleGlnLysLeuIleLysLeuGlnAspMet 144
    ::||::: ||||| ||| ||| |||
Db 1621 CTGAACGATGCTCTGACAGCATGTACAAATGCTGAGAAAGGGAAGGCCCAATCATG 1680

QY 145 GlnLysLysAlaAsnProSerSerLeuValLeuGlnArgGlnValGlnGlnGlnGly 164
    ||||| ||||| :::::
Db 1681 -----ATTGCGCATTCCTCCAAAGTCATTATCATTCCTTTGCTGATCGCAAG 1731

QY 165 PheLeuHisLeuGlnHisAspLysSerLeuAspLeuArgSerArgSerValGln 184
    ::::: ||||| ||| ||| |||
Db 1732 CACGGATACATTTGAGAGTTTGAGTATGTTGATGACACAGGGCTGTAAATCGTGGTT 1791

QY 185 GlnGlyAsnProArg 189
    ||| ||| |||
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